n/a.

RAW SEQUENCE LISTING ERROR REPORT APR 1 7 2000

BIOTECHNOLOGY SYSTEMS BRANCH

TEGRICENTER 1::00/290

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09//86, 869

Art Unit / Team No.: /634

Date Processed by STIC: 5/20/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

| | ERROR DETECTED | SUGGESTED CORRECTION SERIAL NUMBER: 09/186,869 | |
|------------|----------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| ATTN: 1 | NEW RULES CASES: P Wrapped Nucleics | LEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". | |
| 2 | Wrapped Aminos | The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". | |
| 3 | Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. | |
| 4 | Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. | |
| 5 | Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed. | |
| 6 | Variable Length | Sequence(s) contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. | |
| 7 | Patentin ver. 2:0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. | |
| 8 | Skipped Sequences (OLD RULES) | Sequence(s) missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). | ·") |
| 9 | Skipped Sequences (NEW RULES) | Sequence(s) missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000 | |
| 10 | Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. | |
| 11 | Use of <213>Organism (NEW RULES) | Sequence(s) are missing this mandatory field or its response. | |
| 12 | Use of <220>Feature (NEW RULES) | Sequence(s) are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rule) | es) |
| 13 | Patentin ver. 2.0 "bug" | Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. AKS-Biotechnology Systems Branch- 5/15/99 | |



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43

44

<400> 4

RAW SEQUENCE LISTING PATENT APPLICATION US/09/186,869 DATE: 05/20/1999

TIME: 11:46:38

Input Set: I186869.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

Does Not Comply Corrected Diskette Needed <110> Hasel, Karl W. 1 Hilbush, Brian S. 2 <120> Method For Indexing And Determining 3 The Relative Concentration Of Expressed Messenger RNAs <130> 98,429 Le sout a Land return after 51, so that the

"2170" numeri

I sequence

on of Artificial Sequence: synthetic

response of Artificial Sequence: synthetic

margin; <140> US/09/186,869 7 <141> 1998-11-04 <160> 51 8 9 <210> 1 <211> 14 10 11 <212> DNA 12 <213> Artificial Sequence 13 <223> Description of Artificial Sequence:synthetic 14 primer 15 16 <400> 1 14 17 aactggaaga attc 18 <210> 2 19 <211> 14 20 <212> DNA 21 <213> Artificial Sequence 22 <223> Description of Artificial Sequence:synthetic 23 24 primer 25 <400> 2 14 26 gaattcaact ggaa <210> 3 27 <211> 46 28 29 <212> DNA 30 <213> Artificial Sequence 31 <223> Description of Artificial Sequence:synthetic 32 primer 33 34 <400> 3 aactggaaga attcgcggcc gcaggaattt tttttttt tttttv 46 35 36 <210> 4 37 <211> 47 <212> DNA 38 <213> Artificial Sequence 39 40 <220> aactggaaga attcgcggcc gcaggaattt tttttttt ttttttt tttttvm furnavy fleet <223> Description of Artificial Sequence:synthetic 41 42

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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/186,869

DATE: 05/20/1999 TIME: 11:46:38

Input Set: I186869.RAW

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                   primer
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PATENT APPLICATION US/09/186,869

Input Set: I186869.RAW

DATE: 05/20/1999

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DATE: 05/20/1999

| PAGE: | 4 | i | PATENT APPLICATION US/09/186 | ,869 | | | 05/20/ 11:46: | |
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| | 163 | | Description of Artificial Company amthatia | | | | | |
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| | 165 | <400> | | | | | | |
| W> | 166 | (400) | aggtcgacgg tatcggnnn | | | 19 | | |
| " - | 167 | <210> | | | | 19 | | |
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| | 169 | <212> | | | | | | |
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| | 171 | <220> | | | | | | |
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| | 180 | <220> | | | | | | |
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| W> | 184 | | aggtcgacgg tatcggnnnn n | | | 2 | 21 | |
| | 185 | <210> | | | | | | |
| | 186 | <2115 | 22 | | | | | |

RAW SEQUENCE LISTING

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186 <211> 22

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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/186,869

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Input Set: I186869.RAW

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|----|-----|-------|----------------------------------------------|----|
| | 192 | <400> | 20 | |
| | 191 | | primer | |
| | 190 | <223> | Description of Artificial Sequence:synthetic | |
| | 189 | <220> | | |
| | 188 | <213> | Artificial Sequence | |
| | 187 | <212> | DNA | |

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I186869.RAW

| Li | ne | ? | Error/Warning | | | | | Original Text | | | | | |
|----|-------|--------|---------------|----------|--------|---------|-----------|---------------|--|------------|------------|------------|---------|
| | 8 | - E | # of | £ Se | eq. 51 | 17020 I | Not Equal | l Actual 51 | | <160> 51 | | | |
| | | | | | _ | | | required | | aactggaaga | attcgcggcc | gcaggaattt | ttttttt |
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| | | | | | | | | required | | gaattcaact | ggaagcggcc | cgcaggaatt | ttttttt |
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| ; | 148 | W | "N" | or | "Xaa" | used: | Feature | required | | aggtcgacgg | tatcggn | | |
| ; | 157 | W | "N" | or | "Xaa" | used: | Feature | required | | aggtcgacgg | tatcggnn | | |
| : | 166 | W | "N" | or | "Xaa" | used: | Feature | required | | aggtcgacgg | tatcggnnn | | |
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| : | 184 | W | "N" | or | "Xaa" | used: | Feature | required | | aggtcgacgg | tatcggnnnn | n | |
| : | 193 | W | "N" | or | "Xaa" | used: | Feature | required | | aggtcgacgg | tatcggnnnn | nn | |
| : | 211 | W | "N" | or | "Xaa" | used: | Feature | required | | ggtcgacggt | atcggn | 16 | |
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| : | 274 | W | "N" | or | "Xaa" | used: | Feature | required | | gctctgtggt | gaggatcn | | 18 |
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| ; | 301 | W | "N" | or | "Xaa" | used: | Feature | required | | ctgtggtgag | gatcnnnn | | 18 |
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| | 337 | W | "N" | or | "Xaa" | used: | Feature | required | | cgactgtggt | gagcatgn | | 18 |
| ; | 346 | W | "N" | or | "Xaa" | used: | Feature | required | | gactgtggtg | agcatgnn | | 18 |
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| : | 373 | W | "N" | or | "Xaa" | used: | Feature | required | | tgtggtgagc | atgnnnnn | | 18 |
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| 4 | 454 | W | "N" | or | "Xaa" | used: | Feature | required | | gtcttcagtc | aggctaatcg | gn 2 | 2 . |
| 4 | 463 | W | "N" | or | "Xaa" | used: | Feature | required | | cctcgaggtc | gacggtatcg | gn 2 | 2 |